

SUBSTITUTE SEQUENCE LISTING

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<120> METHOD OF GENETIC MODIFICATION OF A WILD
TYPE VIRAL SEQUENCE

<130> VANM190.001APC

<140> US 09/743,905
<141> 2001-04-24

<150> EP 98870159.5
<151> 1998-07-10

<150> PCT BE99/00089
<151> 1999-07-09

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
<223> genetically modified TGB-3 viral sequence

<221> CDS
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Met Val Leu Val Val Ala Val Ala Leu Ser Asn Ile Val Leu Tyr Ile
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gtt gcc act tct gtt gtt gtc agt atg ala tac tca cag ttt ttc agc 96
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
20 25 30
aac gat gtt aaa cgg tcc agc tat gag gga gca att ttt aag ggg agc 144
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
35 40 45
gga tct atc atg cac aac aat tct tct gat gaa ttt ttt agt tta gat 192
Gly Cys Ile Met Asp Asn Asn Ser Phe Ala Glu Phe Gly Ser Lys Asp
50 55 60
att cca aag tat gta gtt gaa tct atc att gag ttt ttt acc aac gag 240
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
65 70 75

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cac cat gac aac ata atg gta aaa agg gat gaa gtg aac gac gat gac 288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
      85      90      95

gtg aac atc acc gaa aat att ttt ata ata tta tct aga ttg ttt ggt 386
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
      100      105      110

ttg gac gtg ttt ttg ttc atg ata tgt tta atg tct ata gac tgg ttc 384
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
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tgg tat cat aga taa 399
Trp Tyr His Arg *
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<220>
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Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
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Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
  35          40          45
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
  50          55          60
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
  65          70          75          80
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
  85          90          95
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
  100          105          110
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
  115          120          125
Trp Tyr His Arg
  130

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<220>
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<230> CDS
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gtt gcc ggt tgt gtt gtt gtc agt atg ttg tac tca cgg ttt ttc agc	96
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser	
20 25 30	
aac gat gtt aaa ggg tcc agc tat ggg gga gca att ttt aag ggg agc	144
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser	
35 40 45	
ggc tgt atc atc ggc ggg aat tgg ttt gct caa ttt ggg agt tgc gat	192
Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp	
50 55 60	
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Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu	
65 70 75 80	
cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt	288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val	
85 90 95	
gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt	336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly	
100 105 110	
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115 120 125	
tgg tat cat aga taa	399
Trp Tyr His Arg *	
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0211> 132

0212> PRT

0213> Artificial Sequence

0220>

0220> genetically modified TCR-3 viral sequence

0400> 4

Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile	
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20 25 30	
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser	
35 40 45	
Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp	
50 55 60	
Ile Phe Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu	
65 70 75 80	
His Asp Val Asp Ile Met Val Lys Arg Gly Gln Val Thr Val Arg Val	
85 90 95	

Val Thr Leu Thr Glu Thr Ile Pro Ile Ile Leu Ser Arg Leu Phe Gly
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 115 120 125
 Trp Tyr His Arg
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<210> 5
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<220>
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<221> CDS
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 gtt ccc ggt tgt gtt gtt gtc agt atg ttg tac tca ccg ttt ttc agc 96
 Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser
 20 25 30
 aac gat gtt aaa ggc tcc agc tat ggc gga gca att ttt aag ggg agc 144
 Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser
 35 40 45
 ggc tgt atc atg gac agg aat tgg ttt gct caa ttt ggg agt tgc gat 192
 Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp
 50 55 60
 att cca aag cat gta gcc gag tcc atc act aag gtt gcc acc aaa gag 240
 Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu
 65 70 75 80
 cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt 288
 His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val
 85 90 95
 gtg act ctc acc gaa act att ttt ata ata tta tot aga ttg ttt ggt 336
 Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly
 100 105 110
 ttg cat gat ttt ttg ttc atg ata tgt tta atg tot ata gtt tga ttt 384
 Leu Asp Asp Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe
 115 120 125
 tgg cat cat aaa aaa 399
 Trp Tyr His Arg
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<410> 5

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<212> PKT

<213> Artificial Sequence

<220>

<223> genetically modified TGB-3 viral sequence

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Met	Val	Leu	Val	Val	Lys	Val	Asp	Leu	Ser	Asn	Ile	Val	Leu	Tyr	Ile	1	5	10	15
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Asn	Asp	Val	Lys	Ala	Ser	Ser	Tyr	Ala	Gly	Ala	Ile	Phe	Lys	Gly	Ser	35	40	45	
Gly	Cys	Ile	Met	Asp	Arg	Asn	Ser	Phe	Ala	Gln	Phe	Gly	Ser	Cys	Asp	50	55	60	
Ile	Pro	Lys	His	Val	Ala	Glu	Ser	Ile	Thr	Lys	Val	Ala	Thr	Lys	Glu	65	70	75	80
His	Asp	Val	Asp	Ile	Met	Val	Lys	Arg	Gly	Glu	Val	Thr	Val	Arg	Val	85	90	95	
Val	Thr	Leu	Thr	Glu	Thr	Ile	Phe	Ile	Ile	Leu	Ser	Arg	Leu	Phe	Gly	100	105	110	
Leu	Asp	Asp	Phe	Leu	Phe	Met	Ile	Cys	Leu	Met	Ser	Ile	Val	Trp	Phe	115	120	125	
Trp	Tyr	His	Arg													130			